



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 08:09 PM UTC

PDB ID : 8BEA / pdb\_00008bea  
Title : Crystal structure of SOS1-HRas-peptidomimetic10  
Authors : Fischer, B.; Wohlkonig, A.; Steyaert, J.  
Deposited on : 2022-10-21  
Resolution : 2.47 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

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<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

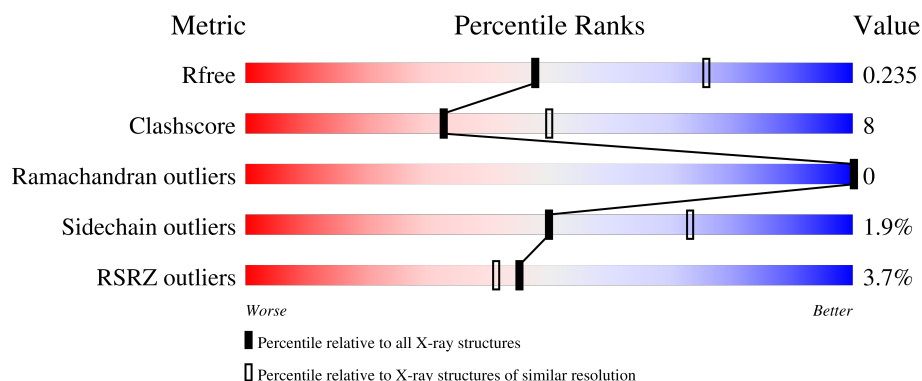
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

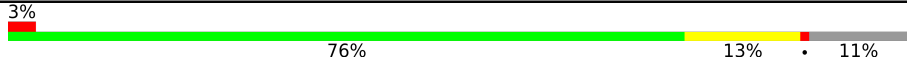
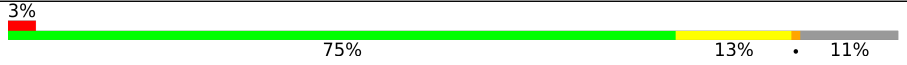
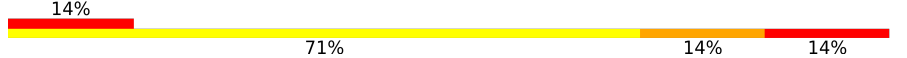
The reported resolution of this entry is 2.47 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	R	186	
2	S	507	
3	P	7	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	VDE	P	1	-	X	-	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5554 atoms, of which 68 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called GTPase HRas.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	166	Total	C	N	O	S	0	0	0
			1322	824	228	263	7			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-19	MET	-	initiating methionine	UNP P01112
R	-18	GLY	-	expression tag	UNP P01112
R	-17	SER	-	expression tag	UNP P01112
R	-16	SER	-	expression tag	UNP P01112
R	-15	HIS	-	expression tag	UNP P01112
R	-14	HIS	-	expression tag	UNP P01112
R	-13	HIS	-	expression tag	UNP P01112
R	-12	HIS	-	expression tag	UNP P01112
R	-11	HIS	-	expression tag	UNP P01112
R	-10	HIS	-	expression tag	UNP P01112
R	-9	SER	-	expression tag	UNP P01112
R	-8	SER	-	expression tag	UNP P01112
R	-7	GLY	-	expression tag	UNP P01112
R	-6	LEU	-	expression tag	UNP P01112
R	-5	VAL	-	expression tag	UNP P01112
R	-4	PRO	-	expression tag	UNP P01112
R	-3	ARG	-	expression tag	UNP P01112
R	-2	GLY	-	expression tag	UNP P01112
R	-1	SER	-	expression tag	UNP P01112
R	0	HIS	-	expression tag	UNP P01112

- Molecule 2 is a protein called Son of sevenless homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	S	449	Total	C	N	O	S	0	1	0
			3749	2412	646	677	14			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	543	MET	-	initiating methionine	UNP Q07889
S	544	GLY	-	expression tag	UNP Q07889
S	545	SER	-	expression tag	UNP Q07889
S	546	SER	-	expression tag	UNP Q07889
S	547	HIS	-	expression tag	UNP Q07889
S	548	HIS	-	expression tag	UNP Q07889
S	549	HIS	-	expression tag	UNP Q07889
S	550	HIS	-	expression tag	UNP Q07889
S	551	HIS	-	expression tag	UNP Q07889
S	552	HIS	-	expression tag	UNP Q07889
S	553	SER	-	expression tag	UNP Q07889
S	554	SER	-	expression tag	UNP Q07889
S	555	GLY	-	expression tag	UNP Q07889
S	556	LEU	-	expression tag	UNP Q07889
S	557	VAL	-	expression tag	UNP Q07889
S	558	PRO	-	expression tag	UNP Q07889
S	559	ARG	-	expression tag	UNP Q07889
S	560	GLY	-	expression tag	UNP Q07889
S	561	SER	-	expression tag	UNP Q07889
S	562	HIS	-	expression tag	UNP Q07889
S	563	MET	-	expression tag	UNP Q07889

- Molecule 3 is a protein called SOS1-HRas-peptidomimetic10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	7	Total	C	H	N	O	0	0	0
			146	51	68	18	9			

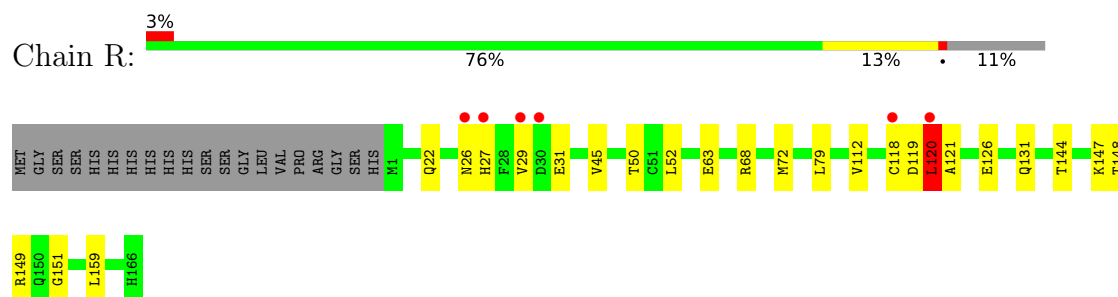
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	R	105	Total	O	0	0
			105	105		
4	S	230	Total	O	0	0
			230	230		
4	P	2	Total	O	0	0
			2	2		

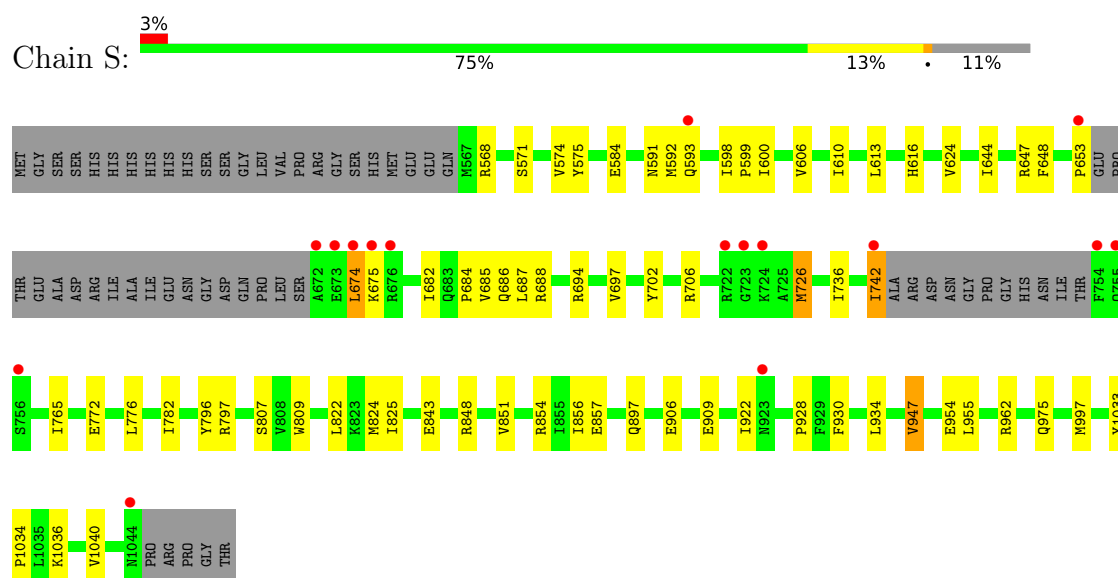
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

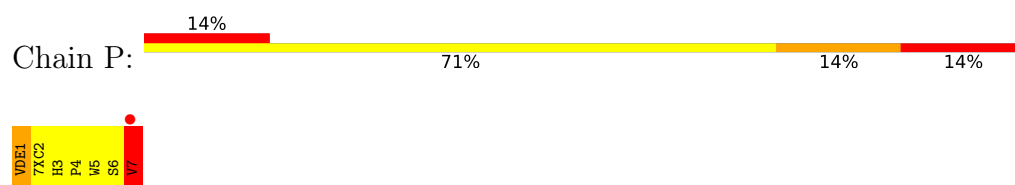
- Molecule 1: GTPase HRas



- Molecule 2: Son of sevenless homolog 1



- Molecule 3: SOS1-HRas-peptidomimetic10



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	150.32Å 150.32Å 203.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.66 – 2.47 48.66 – 2.47	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.66-2.47) 99.6 (48.66-2.47)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.09 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.188 , 0.233 0.191 , 0.235	Depositor DCC
$R_{free}$ test set	2093 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.4	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 34.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.004 for -1/2*h+1/2*k-1/2*l,1/2*h-1/2*k-1/2*l,-h-k 0.001 for -1/2*h-1/2*k+1/2*l,-1/2*h-1/2*k-1/2*l,h-k	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5554	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 7XC, VDE

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	R	0.60	0/1341	0.84	1/1810 (0.1%)
2	S	0.58	0/3840	0.75	2/5191 (0.0%)
3	P	4.26	7/47 (14.9%)	2.43	2/65 (3.1%)
All	All	0.71	7/5228 (0.1%)	0.81	5/7066 (0.1%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	4	PRO	C-N	14.42	1.52	1.33
3	P	6	SER	C-N	14.04	1.53	1.33
3	P	5	TRP	C-N	10.23	1.47	1.33
3	P	3	HIS	C-N	8.52	1.44	1.33
3	P	3	HIS	CG-ND1	-6.71	1.30	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S	591	ASN	CA-C-N	-6.71	113.20	122.93
2	S	591	ASN	C-N-CA	-6.71	113.20	122.93
3	P	3	HIS	CA-CB-CG	-6.43	107.37	113.80
3	P	7	VAL	CA-C-O	-5.92	110.74	120.80
1	R	120	LEU	N-CA-C	-5.02	107.15	113.28

There are no chirality outliers.

There are no planarity outliers.



## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	1322	0	1296	26	0
2	S	3749	0	3781	52	0
3	P	78	68	38	5	0
4	P	2	0	0	0	0
4	R	105	0	0	3	0
4	S	230	0	0	3	0
All	All	5486	68	5115	81	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 81 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:687:LEU:HD23	2:S:726:MET:HE1	1.37	1.07
2:S:687:LEU:CD2	2:S:726:MET:HE1	1.91	1.00
2:S:682:ILE:O	2:S:686:GLN:HG3	1.74	0.88
1:R:22:GLN:NE2	1:R:149:ARG:HG2	1.92	0.84
2:S:687:LEU:HD23	2:S:726:MET:CE	2.11	0.81

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	R	164/186 (88%)	159 (97%)	5 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	S	444/507 (88%)	435 (98%)	9 (2%)	0	100	100
3	P	4/7 (57%)	4 (100%)	0	0	100	100
All	All	612/700 (87%)	598 (98%)	14 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	144/161 (89%)	142 (99%)	2 (1%)	59	79
2	S	422/469 (90%)	414 (98%)	8 (2%)	50	73
3	P	5/5 (100%)	4 (80%)	1 (20%)	1	2
All	All	571/635 (90%)	560 (98%)	11 (2%)	50	73

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	S	772	GLU
2	S	930	PHE
3	P	7	VAL
2	S	947	VAL
2	S	675	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	S	888	HIS
2	S	972	GLN
2	S	1020	ASN
2	S	993	ASN
2	S	593	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	7XC	P	2	3	14,15,16	3.44	7 (50%)	13,19,21	1.55	3 (23%)
3	VDE	P	1	3	18,19,20	3.54	8 (44%)	19,24,26	3.47	11 (57%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	7XC	P	2	3	-	1/9/10/12	0/1/1/1
3	VDE	P	1	3	-	11/16/17/19	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	1	VDE	C25-C24	9.90	1.52	1.36
3	P	2	7XC	C10-N2	8.54	1.49	1.38
3	P	1	VDE	C72-N3	6.23	1.47	1.32
3	P	2	7XC	C10-N4	5.31	1.53	1.34
3	P	1	VDE	C71-C24	4.66	1.62	1.49

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	1	VDE	N21-N22-N23	6.05	112.47	107.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	1	VDE	C20-N21-N22	5.38	131.58	120.78
3	P	1	VDE	C25-N21-N22	-5.31	105.58	110.75
3	P	1	VDE	C71-C24-N23	5.03	129.31	121.75
3	P	1	VDE	C70-C72-N3	4.84	125.01	116.75

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	P	1	VDE	C18-C17-CA-C
3	P	1	VDE	C18-C17-CA-N
3	P	1	VDE	N2-C70-C72-N3
3	P	1	VDE	C18-C19-C20-N21
3	P	1	VDE	C17-C18-C19-C20

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	P	1	VDE	4	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	R	166/186 (89%)	-0.21	6 (3%) 46 42	31, 39, 65, 87	0
2	S	449/507 (88%)	-0.02	16 (3%) 46 42	22, 44, 77, 107	1 (0%)
3	P	5/7 (71%)	0.80	1 (20%) 3 2	47, 49, 67, 87	0
All	All	620/700 (88%)	-0.07	23 (3%) 45 41	22, 43, 76, 107	1 (0%)

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	R	120	LEU	6.3
2	S	672	ALA	6.3
2	S	673	GLU	6.2
2	S	754	PHE	4.2
1	R	27	HIS	4.2

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	VDE	P	1	19/20	0.59	0.17	77,97,109,113	0
3	7XC	P	2	15/16	0.88	0.11	62,69,83,86	0

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.